Sequence Match Listing
for 09/954987

RESULT 6
BE705670/c
LOCUS BE705670 737 bp mRNA linear EST 12-SEP-2000
DEFINITION Sc01_11a10_A Sc01_AAFC_ECORC_cold_stressed_winter_rye_seedlings Secale cereale cDNA clone Sc01_11a10, mRNA sequence.
ACCESSION BE705670
VERSION BE705670.1 GI:10093935
KEYWORDS EST.
SOURCE rye.
ORGANISM Secale cereale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Secale.
REFERENCE 1 (bases 1 to 737)
AUTHORS Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
TITLE Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
JOURNAL Unpublished (2000)
COMMENT Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A 0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
FEATURES Location/Qualifiers
source 1. .737
/organism="Secale cereale"
/cultivar="Puma (winter rye)"
/db_xref="taxon:4550"
/clone="Sc01_11a10"
/clone_lib="Sc01_AAFC_ECORC_cold_stressed_winter_rye_seedlings"
/tissue_type="leaf, crown"
/dev_stage="seedling three-leaf stage"
/note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI; Site_2: Xho I; Sampled three-leaf seedlings treated for one week at 2oC, 12 hrs light/day. Library made with Stratagene UNIZAP XR Kit/Gigapack III Gold Kit. Lambda library is amplified, then mass excised in SOLR cells. "
BASE COUNT 156 a 189 c 200 g 170 t 22 others
ORIGIN

Query Match 55.1%; Score 24.8; DB 12; Length 737;
Best Local Similarity 80.6%; Pred. No. 46;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 CTGCATGGAGTGCGGCCAAAAGTCCCTCCACCTACA 36
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Db        549 CTGAGTGGAGGGCGGCCAAGAGCCCCTCCTACTACA 514
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530 531

RESULT 7

BE412777
LOCUS BE412777 928 bp mRNA linear EST 24-JUL-2000
DEFINITION MCG008.H03R990625 ITEC MCG Barley Leaf/Culm Library Hordeum vulgare cDNA clone MCG008.H03, mRNA sequence.
ACCESSION BE412777
VERSION BE412777.1 GI:9410525
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 928)
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier ,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
TITLE International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
JOURNAL Unpublished (2000)
COMMENT Contact: Graner A
Institute for Plant Genetics & Crop Plant Research
Correnssstr. 3, D-06466 Gatersleben GERMANY
Tel: 49 39482 5521
Fax: 49 39482 5137
Email: a_graner@ipk-gatersleben.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
FEATURES Location/Qualifiers
source 1. .928
/organism="Hordeum vulgare"
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/clone_lib="ITEC MCG Barley Leaf/Culm Library"
/tissue_type="leaf/culm"
/dev_stage="etiolated"
BASE COUNT 237 a 181 c 247 g 254 t 9 others
ORIGIN

Query Match 55.1%; Score 24.8; DB 10; Length 928;
Best Local Similarity 80.6%; Pred. No. 48;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 CTGCATGGAGTGCGGCCAAAAGTCCCTCCACCTACA 36
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Db         86 CTGAGTGGAGGGCGGCCAAGAGCCCCTCCTACTACA 121
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99 104

RESULT 13
AQ984126/c
LOCUS AQ984126 503 bp DNA linear GSS 30-JAN-2000
DEFINITION RPCI-23-306D11.TV RPCI-23 Mus musculus genomic clone RPCI-23-306D11
, DNA sequence.
ACCESSION AQ984126
VERSION AQ984126.1 GI:6817331
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 503)
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-23-306D11.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 306 row: D column: 11
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1. .503
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-306D11"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
BASE COUNT 144 a 125 c 127 g 107 t
ORIGIN

Query Match 51.6%; Score 23.2; DB 17; Length 503;
Best Local Similarity 70.5%; Pred. No. 1.7e+02;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 2 TGCATGGAGTGCGGCCAAAAGTCCCTCCACCTACATCCCGATAC 45
Db 385 TACATGGACCCAGGCCAACAGTTCTTCTCCCCACATCCGGAGAC 342

375 378

RESULT 13
T49841
hypothetical protein B24H17.270 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T49841
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49841
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-218 <SCH>
A;Cross-references: EMBL:AL356815; GSPDB:GN00116; NCSP:B24H17.270
A;Experimental source: BAC clone B24H17; strain OR74A
C;Genetics:
A;Gene: NCSP:B24H17.270
A;Map position: 6
A;Introns: 8/1; 107/1; 144/1; 180/2
C;Superfamily: Neurospora crassa hypothetical protein B24H17.270

  Query Match   38.5%; Score 48.5; DB 2; Length 218;
  Best Local Similarity 52.9%; Pred. No. 21;
  Matches   9; Conservative   2; Mismatches   5; Indels   1; Gaps   1;

Qy   3 RCDHAPNPCME-CGQKS 18
              : || ||: |||||
Db   40 QADHGNEPCLPVCGQKS 56

earliest date June 21 2000

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RESULT 2
AF245704
LOCUS       AF245704               3352 bp    mRNA    linear   PRI 21-MAR-2001
DEFINITION  Homo sapiens toll-like receptor 9 (TLR9) mRNA, complete cds.
ACCESSION   AF245704
VERSION     AF245704.1  GI:8575528
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3352)
  AUTHORS   Chuang,T.H. and Ulevitch,R.J.
  TITLE     Cloning and characterization of a sub-family of human toll-like
            receptors: hTLR7, hTLR8 and hTLR9
  JOURNAL   Eur. Cytokine Netw. 11 (3), 372-378 (2000)
  MEDLINE   20477807
   PUBMED   11022120
REFERENCE   2  (bases 1 to 3352)
  AUTHORS   Chuang,T.-H.H. and Ulevitch,R.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2000) Immunology, The Scripps Research Institute,
            10550 North Torrey Pines Road, La Jolla, CA 92037, USA
FEATURES             Location/Qualifiers
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                     /chromosome="3"
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     gene            1. .3352
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     CDS             145. .3243
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                     ASLAGLHALRFLFMDGNCYYKNPCRQALEVAPGALLGLGNLTHLSLKYNNLTVVPRNL
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                     SQAVNGSQFLPLTGLQVLDLSRNKLDLYHEHSFTELPRLEALDLSYNSQPFGMQGVGH
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                     DLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAPGFFSKAKELRELNLSANALKTV
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                     LSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHLCGWDLWYCFHLCLAWLPW
                     RGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRGRWALRLCLEERDWL
                     PGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLEDRKDVVVLVILS
                     PDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHHFYNRNFCQGPT
                     AE"
BASE COUNT      585 a   1196 c    891 g    680 t
ORIGIN

  Query Match           99.5%;  Score 3080;  DB 9;  Length 3352;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 3086;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTG 60
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Db        145 ATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTG 204

Qy         61 GCCATGACCCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCAC 120
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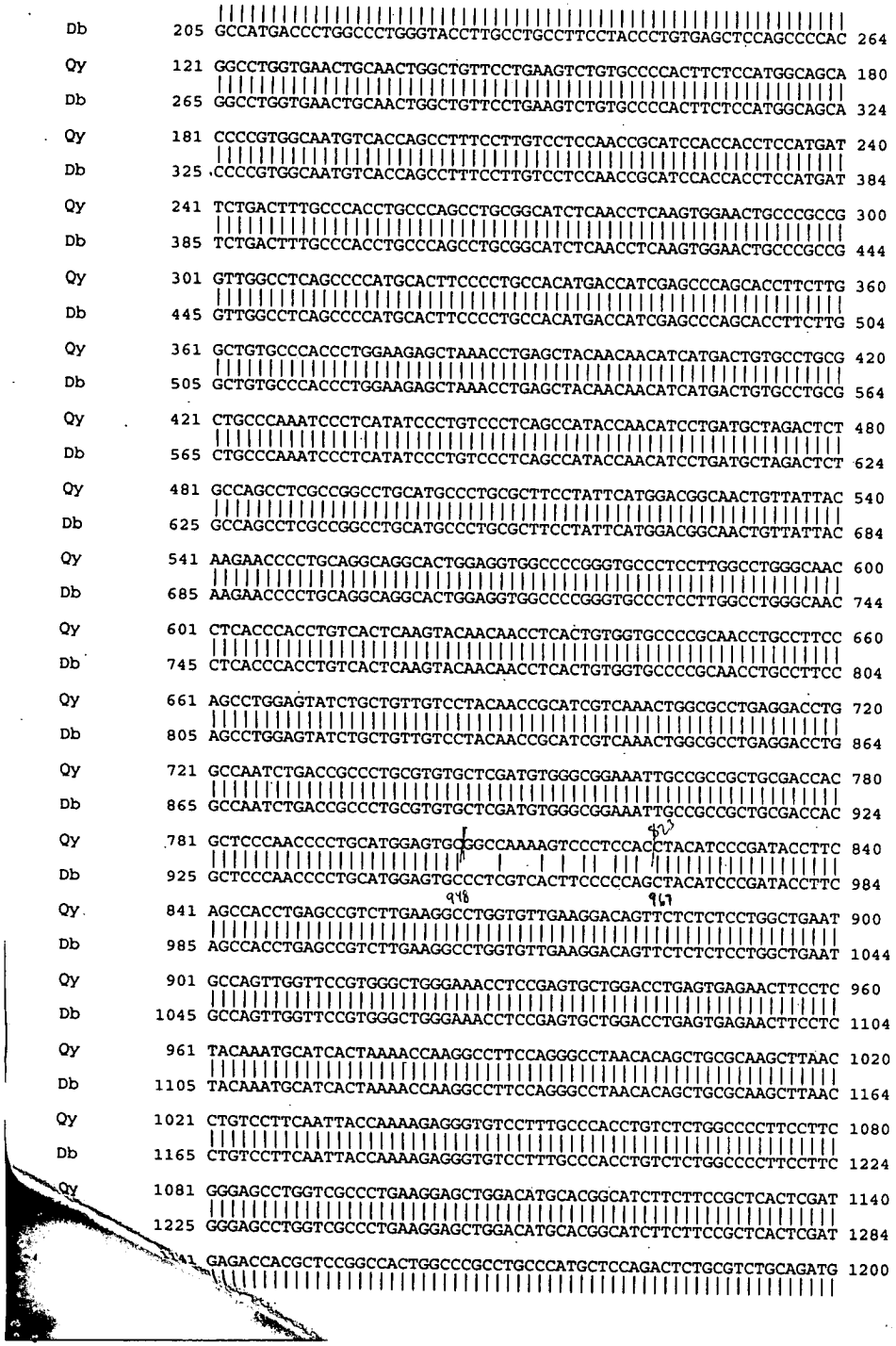
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Db 265 GGCCTGGTGAACTGCAACTGGCTGTTCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCA 324
Qy 181 CCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGCATCCACCACCTCCATGAT 240
Db 325 CCCCGTGGCAATGTCACCAGCCTTTCCTTGTCCTCCAACCGCATCCACCACCTCCATGAT 384
Qy 241 TCTGACTTTGCCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCCG 300
Db 385 TCTGACTTTGCCCCACCTGCCCAGCCTGCGGCATCTCAACCTCAAGTGGAACTGCCCGCCG 444
Qy 301 GTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTG 360
Db 445 GTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTG 504
Qy 361 GCTGTGCCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCG 420
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Qy 421 CTGCCCAAATCCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCT 480
Db 565 CTGCCCAAATCCCTCATATCCCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCT 624
Qy 481 GCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCTATTCATGGACGGCAACTGTTATTAC 540
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Qy 541 AAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGGCCTGGGCAAC 600
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Qy 601 CTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCC 660
Db 745 CTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGCCCCGCAACCTGCCTTCC 804
Qy 661 AGCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTG 720
Db 805 AGCCTGGAGTATCTGCTGTTGTCCTACAACCGCATCGTCAAACTGGCGCCTGAGGACCTG 864
Qy 721 GCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCAC 780
Db 865 GCCAATCTGACCGCCCTGCGTGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCAC 924
Qy 781 GCTCCCAACCCCTGCATGGAGTGCGGCCAAAAGTCCCTCCACCTACATCCCGATACCTTC 840
Db 925 GCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTTCCCCCAGCTACATCCCGATACCTTC 984
Qy 841 AGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAAT 900
Db 985 AGCCACCTGAGCCGTCTTGAAGGCCTGGTGTTGAAGGACAGTTCTCTCTCCTGGCTGAAT 1044
Qy 901 GCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTC 960
Db 1045 GCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCCTC 1104
Qy 961 TACAAATGCATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAAC 1020
Db 1105 TACAAATGCATCACTAAAACCAAGGCCTTCCAGGGCCTAACACAGCTGCGCAAGCTTAAC 1164
Qy 1021 CTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTC 1080
Db 1165 CTGTCCTTCAATTACCAAAAGAGGGTGTCCTTTGCCCACCTGTCTCTGGCCCCTTCCTTC 1224
Qy 1081 GGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGAT 1140
Db 1225 GGGAGCCTGGTCGCCCTGAAGGAGCTGGACATGCACGGCATCTTCTTCCGCTCACTCGAT 1284
Db 1285 GAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCGTCTGCAGATG 1344
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Db 1345 AACTTCATCAACCAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTG 1404
Qy 1261 GACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCA 1320
Db 1405 GACCTGTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCA 1464
Qy 1321 GATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACT 1380
Db 1465 GATGGAGGGGAGAAGGTCTGGCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACT 1524
Qy 1381 CCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCA 1440
Db 1525 CCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCACCCTCAACTTCACCTTGGATCTGTCA 1584
Qy 1441 CGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGC 1500
Db 1585 CGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCCAGCTCTCGCACCTGCAGTGC 1644
Qy 1501 CTGCGCCTGAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTG 1560
Db 1645 CTGCGCCTGAGCCACAACTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCCTGCCGCTG 1704
Qy 1561 ACCGGTCTGCAGGTGCTAGACCTGTCCCGCAATAAGCTGGACCTCTACCACGAGCACTCA 1620
Db 1705 ACCGGTCTGCAGGTGCTAGACCTGTCCCGCAATAAGCTGGACCTCTACCACGAGCACTCA 1764
Qy 1621 TTCACGGAGCTACCGCGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGC 1680
Db 1765 TTCACGGAGCTACCGCGACTGGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGC 1824
Qy 1681 ATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTC 1740
Db 1825 ATGCAGGGCGTGGGCCACAACTTCAGCTTCGTGGCTCACCTGCGCACCCTGCGCCACCTC 1884
Qy 1741 AGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTG 1800
Db 1885 AGCCTGGCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAGTACGTCGCTG 1944
Qy 1801 CGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTAT 1860
Db 1945 CGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTAT 2004
Qy 1861 CTGCACTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCGCCTG 1920
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Qy 1921 CACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTC 1980
Db 2065 CACACCCTCCTGCCCCAAACCCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTC 2124
Qy 1981 CGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAGCCTCCACTTCCTGCCCAAACTGGAA 2040
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Qy 2041 GTCCTCGACCTGGCAGGAAACCGGCTGAAGGCCCTGACCAATGGCAGCCTGCCTGCTGGC 2100
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Qy 2101 ACCCGGCTCCGGAGGCTGGATGTCAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTC 2160
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Qy 2161 TTTTCCAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTG 2220
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Qy 2221 GACCACTCCTGGTTTGGGCCCCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAAC 2280
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Qy      2281 CCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCC 2340
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Db      2425 CCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCC 2484

Qy      2341 GTGCCCGGTCTGCCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCAGGGCCTCAGC 2400
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Db      2485 GTGCCCGGTCTGCCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCAGGGCCTCAGC 2544

Qy      2401 ATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCC 2460
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Db      2545 ATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCC 2604

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Db      2605 CTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGC 2664

Qy      2521 TGGGACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAA 2580
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Db      2665 TGGGACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAA 2724

Qy      2581 AGTGGGCGAGATGAGGATGCCCTGCCCTACGATGCCTTCGTGGTCTTCGACAAAACGCAG 2640
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Qy      2641 AGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGGAGGAGTGCCGTGGG 2700
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Db      2785 AGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGGAGGAGTGCCGTGGG 2844

Qy      2701 CGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCTCTTT 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      2761 GAGAACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCACACG 2820
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Qy      2821 GACCGGGTCAGTGGTCTCTTGCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAG 2880
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Qy      2881 GACCGCAAGGACGTCGTGGTGCTGGTGATCCTGAGCCCTGACGGCCGCCGCTCCCGCTAC 2940
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Qy      2941 GTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAGCCCAGT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3085 GTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAGCCCAGT 3144

Qy      3001 GGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTC 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3145 GGTCAGCGCAGCTTCTGGGCCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTC 3204

Qy      3061 TATAACCGGAACTTCTGCCAGGGACCCACGGCCGAA 3096
             ||||||||||||||||||||||||||||||||||||
Db      3205 TATAACCGGAACTTCTGCCAGGGACCCACGGCCGAA 3240
```